

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule encoding a tyrosine ammonia lyase enzyme, selected from the group consisting of:
 - 5 a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:3;
 - b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS, 65 °C and washed with 2X SSC, 0.1% SDS
 - 10 followed by 0.1X SSC, 0.1% SDS; or
 - an isolated nucleic acid molecule that is complementary to (a) or (b).
2. An isolated nucleic acid molecule as set forth in SEQ ID NO:2.
3. A polypeptide encoded by the isolated nucleic acid molecule of Claim 1.
- 15 4. A polypeptide encoded by the isolated nucleic acid molecule of Claim 2.
5. A polypeptide having the amino acid sequence as set forth in SEQ ID NO:3.
6. An isolated nucleic acid molecule comprising a first nucleotide
 - 20 sequence encoding a polypeptide of at least 526 amino acids that has at least 56% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:3 or a second nucleotide sequence comprising the complement of the first nucleotide sequence, wherein said enzyme has tyrosine ammonia
 - 25 lyase activity.
7. A chimeric gene comprising the isolated nucleic acid molecule of Claims 1 or 2 operably linked to suitable regulatory sequences.
8. A transformed host cell comprising the chimeric gene of Claim 7.
- 30 9. The transformed host cell of Claim 8 wherein the host cell is selected from the group consisting of bacteria, yeast, filamentous fungi, algae, and green plants.
10. The transformed host cell of Claim 9 wherein the host cell is selected from the group consisting of *Escherichia*, *Salmonella*, *Bacillus*,
 - 35 *Acinetobacter*, *Streptomyces*, *Methylobacter*, *Rhodococcus*, *Pseudomonas*, *Rhodobacter*, *Synechocystis*, *Aspergillus* and *Arthrobotrys*.

11. The transformed host cell of Claim 8 wherein the host cell is selected from the group consisting of *Saccharomyces*, *Zygosaccharomyces*, *Kluyveromyces*, *Candida*, *Hansenula*, *Debaryomyces*, *Pichia*, *Mucor*, and *Torulopsis*.

5 12. The transformed host cell of Claim 8 wherein the host cell is selected from the group consisting soybean, rapeseed, pepper, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, rice, *Arabidopsis*, cruciferous vegetables, melons, carrots, celery, parsley, tomatoes, potatoes, strawberries, peanuts, grapes, grass seed crops, 10 sugar beets, sugar cane, beans, peas, rye, flax, hardwood trees, softwood trees, and forage grasses.

13. A method of obtaining a nucleic acid molecule encoding a tyrosine ammonia lyase enzyme comprising:

- 15 a) probing a genomic library with the nucleic acid molecule of any one of Claims 1 or 2;
- b) identifying a DNA clone that hybridizes with the nucleic acid molecule of any one of Claims 1 or 2; and
- c) sequencing the genomic fragment that comprises the clone identified in step (b),

20 wherein the sequenced genomic fragment encodes a tyrosine ammonia lyase enzyme.

14. A method of obtaining a nucleic acid molecule encoding a tyrosine ammonia lyase enzyme comprising:

- 25 a) synthesizing at least one oligonucleotide primer corresponding to a portion of the sequence as set forth in SEQ ID NO:2; and
- b) amplifying an insert present in a cloning vector using the oligonucleotide primer of step (a);

30 wherein the amplified insert encodes a portion of an amino acid sequence encoding a tyrosine ammonia lyase enzyme.

15. The product of the method of Claims 13 or 14.

16. A method for the production of para-hydroxycinnamic acid comprising:

- 35 (a) contacting a recombinant host cell with a fermentable carbon substrate, said recombinant cell comprising the isolated nucleic acid molecule of Claims 1 or 2 operably linked to suitable regulatory sequences;

(b) growing said recombinant cell for a time sufficient to produce para-hydroxycinnamic acid; and

(c) optionally recovering said para-hydroxycinnamic acid.

17. A method according to Claim 16, wherein said fermentable
5 carbon substrate is selected from the group consisting of monosaccharides, oligosaccharides, polysaccharides, carbon dioxide, methanol, formaldehyde, formate, and carbon-containing amines.

18. A method according to Claim 17 wherein said fermentable carbon substrate is glucose.

10 19. A method according to Claim 16 wherein said recombinant host cell is selected from the group consisting of bacteria, yeasts, filamentous fungi, algae and plant cells.

20. A method according to Claim 19 wherein said recombinant host cell is selected from the group consisting of *Aspergillus*, *Arthrotrrys*,
15 *Saccharomyces*, *Zygosaccharomyces*, *Pichia*, *Kluyveromyces*, *Candida*, *Hansenula*, *Debaryomyces*, *Mucor*, *Torulopsis*, *Methylobacter*, *Escherichia*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Rhodococcus*, *Rhodobacter*, *Synechocystis*, *Streptomyces*, and *Pseudomonas*.

21. A method according to Claim 16 wherein said recombinant host
20 cell is selected from the group consisting of soybean, rapeseed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, rice, broccoli, cauliflower, cabbage, parsnips, melons, carrots, celery, parsley, tomatoes, potatoes, strawberries, peanuts, grapes, grass seed crops, sugar beets, sugar cane, beans, peas, rye, flax, hardwood trees,
25 softwood trees, and forage grasses.

22. The method according to Claim 16 wherein said gene encoding a tyrosine ammonia lyase activity encodes the peptide set forth in SEQ ID NO:3.

23. The method according to Claim 16 wherein the gene encoding
30 a tyrosine ammonia lyase activity is derived from *Rhodobacter sphaeroides*.